

Appl. No. 09/889,053
Atty. Docket No. 7379M
Amdt. dated April 12, 2006
Reply to Office Action of January 13, 2006
Customer No. 27752

AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior listing of claims for this application.

1. (Currently amended) A method of ~~determining the amino acid sequence of~~ sequencing a polypeptide characterized in that it comprises polypeptide, said method comprising:

(a) derivatizing ~~[[the]] a N-terminus of [[the]] a polypeptide or the N-termini~~ an N-termini of one or more peptides at least one peptide of the polypeptide with one or more acidic moieties at least one acidic moiety having [[pKas]] a pKa of less than about 2, when coupled with [[the]] a polypeptide or peptides at least one peptide of the polypeptide, to provide one or more at least one derivatized analytes analyte;

(b) analyzing ~~the one or more at least one derivatized analytes analyte~~ using a mass spectrometric technique to provide a fragmentation pattern; and

(c) interpreting the fragmentation pattern.

2. (Currently amended) ~~[[A]] The method according to Claim 1 characterized in that~~ recited in claim 1, wherein the mass spectrometric technique used is MALDI PSD mass spectrometry; or electrospray ionization tandem mass spectrometry.

3. (Currently amended) ~~[[A]] The method according to Claim 2 characterized in that interpretation of~~ recited in claim 1, wherein said step of interpreting the fragmentation pattern further comprises using a commercially available software program or comparing the fragmentation pattern against a database.

4. (Currently amended) ~~[[A]] The method according to Claim 3 characterized in that~~ recited in claim 1, wherein the polypeptide polypeptide is a synthetic polypeptide polypeptide.

5. (Currently amended) ~~[[A]] The method according to Claim 4 characterized in that~~ recited in claim 1, wherein the peptides at least one peptide of the polypeptide [[are]] is produced by enzymatic or chemical digestion.

6. (Canceled).

7. (Currently amended) ~~[[A]] The method according to Claim 6 characterized in that~~ recited in claim 1, wherein the acidic moiety is one or more at least one sulfonic [[acids]] acid or a disulfonic acid derivative.

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8. (Withdrawn) A kit for use in determining the amino acid sequence of a polypeptide characterized in that it comprises:

(a) one or more acidic moiety reagents providing one or more acidic moieties having pKas of less than 2 when coupled with the polypeptide or one or more peptides of the polypeptide; and

(b) means for derivatizing the N-terminus of the polypeptide or the N-termini of one or more peptides of the polypeptide with one or more acidic moiety reagents.

9. (Withdrawn) A kit according to Claim 8 characterized in that the means for derivatizing comprises one or more containment devices.

10. (Withdrawn) A kit according to Claim 9 characterized in that it Mther comprises one or more digestion aids.

11. (New) A method of sequencing a polypeptide, said method comprising:
adding at least one acidic group to the N-terminus of a polypeptide or at least one peptide formed through cleavage of the polypeptide;

coupling the at least one acidic group to the N-terminus, wherein said coupled polypeptide or at least one peptide has a pKa of less than about 2;

providing at least one derivatized analyte with a mass spectra predominantly characterized by y-ions; and

analyzing the at least one derivatized analyte.